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RAW SEQUENCE LISTING   DATE: 01/29/2002
PATENT APPLICATION: US/09/993,756A   TIME: 10:55:29

Input Set : N:\Crf3\RULE60\09993756A.raw
Output Set: N:\CRF3\01292002\I993756A.raw

SEQUENCE LISTING
3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Akerblom, Ingrid E.
7   (ii) TITLE OF INVENTION: A NOVEL HUMAN LEPTIN RECEPTOR
8   GENE-RELATED PROTEIN
10   (iii) NUMBER OF SEQUENCES: 4
12   (iv) CORRESPONDENCE ADDRESS:
13   (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
14   (B) STREET: 3174 Porter Drive
15   (C) CITY: Palo Alto
16   (D) STATE: CA   ENTERED
17   (E) COUNTRY: U.S.
18   (F) ZIP: 94304
20   (v) COMPUTER READABLE FORM:
21   (A) MEDIUM TYPE: Diskette
22   (B) COMPUTER: IBM Compatible
23   (C) OPERATING SYSTEM: DOS
24   (D) SOFTWARE: FastSEQ Version 1.5
26   (vi) CURRENT APPLICATION DATA:
C--> 27   (A) APPLICATION NUMBER: US/09/993,756A
C--> 28   (B) FILING DATE: 05-Nov-2001
30   (vii) PRIOR APPLICATION DATA:
32   (A) APPLICATION NUMBER: US/09/212,153
33   (B) FILING DATE:
34   (A) APPLICATION NUMBER: US/08/843,370
35   (B) FILING DATE:
36   (A) APPLICATION NUMBER: US 08/691,071
37   (B) FILING DATE: August 1, 1996
39   (viii) ATTORNEY/AGENT INFORMATION:
40   (A) NAME: Billings, Lucy J.
41   (B) REGISTRATION NUMBER: 36,749
42   (C) REFERENCE/DOCKET NUMBER: PF-0111-1 US
44   (ix) TELECOMMUNICATION INFORMATION:
45   (A) TELEPHONE: 415-855-0555
46   (B) TELEFAX: 415-845-4166
48 (2) INFORMATION FOR SEQ ID NO: 1:
50   (i) SEQUENCE CHARACTERISTICS:
51   (A) LENGTH: 131 amino acids
52   (B) TYPE: amino acid
53   (C) STRANDEDNESS: single
54   (D) TOPOLOGY: linear
56   (ii) MOLECULE TYPE: peptide
58   (vii) IMMEDIATE SOURCE:

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```
59              (A) LIBRARY: HNT2NOT01
60              (B) CLONE: 492703
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64   Met Ala Gly Val Lys Ala Leu Val Ala Leu Ser Phe Ser Gly Ala Ile
65    1           5                  10                  15
66   Gly Leu Thr Phe Leu Met Leu Gly Cys Ala Leu Glu Asp Tyr Gly Val
67            20                  25                  30
68   Tyr Trp Pro Leu Phe Val Leu Ile Phe His Gly Ile Ser Pro Ile Pro
69            35                  40                  45
70   His Phe Ile Ala Lys Arg Val Thr Tyr Asp Ser Asp Ala Thr Ser Ser
71        50                  55                  60
72   Ala Cys Arg Glu Leu Ala Tyr Phe Phe Thr Thr Gly Ile Val Val Ser
73    65                  70                  75                  80
74   Ala Phe Gly Phe Pro Val Ile Leu Ala Arg Val Ala Val Ile Lys Trp
75                    85                  90                  95
76   Gly Ala Cys Gly Leu Val Leu Ala Gly Asn Ala Val Ile Phe Leu Thr
77                100                 105                 110
78   Ile Gln Gly Phe Phe Leu Ile Phe Gly Arg Gly Asp Asp Phe Ser Trp
79                115                 120                 125
80   Glu Gln Trp
81        130
83 (2) INFORMATION FOR SEQ ID NO: 2:
85       (i) SEQUENCE CHARACTERISTICS:
86           (A) LENGTH: 874 base pairs
87           (B) TYPE: nucleic acid
88           (C) STRANDEDNESS: single
89           (D) TOPOLOGY: linear
91      (ii) MOLECULE TYPE: cDNA
93     (vii) IMMEDIATE SOURCE:
94           (A) LIBRARY: HNT2NOT01
95           (B) CLONE: 492703
97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
99   GTCTGGCTTG GGCAGGCTGC CCGGGCCGTG GCAGGAAGCS GGAAGCAGCC GCGGCCCCAG    60
100  TTCGGGAGAC ATGGCGGGCG TTAAAGCTCT CGTGGCATTA TCCTTCAGTG GGGCTATTGG   120
101  ACTGACTTTT CTTATGCTGG GATGTGCCTT AGAGGATTAT GGCGTTTACT GGCCCTTATT   180
102  CGTCCTGATT TTCCACGGCA TCTCCCCCAT CCCCCATTTC ATTGCCAAAA GAGTCACCTA   240
103  TGACTCAGAT GCAACCAGTA GTGCCTGTCG GGAACTGGCA TATTTCTTCA CTACTGGAAT   300
104  TGTTGTTTCT GCCTTTGGAT TTCCTGTTAT TCTTGCTCGT GTGGCTGTGA TCAAATGGGG   360
105  AGCCTGCGGC CTTGTGTTGG CAGGCAATGC AGTCATTTTC CTTACAATTC AAGGGTTTTT   420
106  CCTTATATTT GGAAGAGGAG ATGATTTTAG CTGGGAGCAG TGGTAGCACT TTATTCTGAT  ·480
107  TACAGTGCAT TGAATTTCTT AGAACTCATA CTATCTGTAT ACATGTGCAC ATGCGGCATT   540
108  TTACTATGAA ATTTAATATG CTGGGTTTTT TAATACCTTT ATATATCATG TTCACTTTAA   600
109  GAAAGACTTC ATAAGTAGGA GATGAGTTTT ATTCTCAGCA AATAGACCTG TCAAATTTAG   660
110  ATTATGTTAC TCAAATTATG TTACTTGTTT GGCTGTTCAT GTAGTCACGG TGCTCTCAGA   720
111  AAATATATTA ACGCAGTCTT GTAGGCAGCT GCCACCTTAT GCAGTGCATC GAAACCTTTT   780
112  GCTTGGGGAT GTGCTTGGAG AGGCAGATAA CGCTGAAGCA GGCCTCTCAT GACCCAGGAA   840
113  GGCCGGGGTG GWTCCCTCTT TKTTTTGTAG TCCA                               874
115 (2) INFORMATION FOR SEQ ID NO: 3:
117       (i) SEQUENCE CHARACTERISTICS:
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```
118              (A) LENGTH: 145 amino acids
119              (B) TYPE: amino acid
120              (C) STRANDEDNESS: single
121              (D) TOPOLOGY: linear
123       (ii) MOLECULE TYPE: peptide
125      (vii) IMMEDIATE SOURCE:
126              (A) LIBRARY: GenBank
127              (B) CLONE: 733888
129       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
131    Met Cys Cys His Ile His Ile Gln Cys Phe Asp Cys Cys Ser Met Lys
132    1               5                  10                  15
133    Asn Thr Ile Leu Ala Val Ala Ala Leu Ala Phe Ala Gly Val Val Gly
134                20                  25                  30
135    Leu Thr Phe Leu Val Leu Gly Cys Ala Leu Pro Arg Tyr Gly Thr Trp
136                35                  40                  45
137    Thr Pro Met Phe Val Ile Thr Phe Tyr Val Leu Ser Pro Val Pro Leu
138        50                  55                  60
139    Leu Ile Ala Arg Arg Phe Gln Glu Asp Met Thr Gly Thr Asn Ala Cys
140    65                  70                  75                  80
141    Ile Glu Leu Ala Leu Phe Ile Thr Thr Gly Ile Val Ile Ser Ala Phe
142                85                  90                  95
143    Ala Leu Pro Ile Val Leu Ala His Ala Gly Thr Ile Ala Met Ser Ala
144                100                 105                 110
145    Cys Phe Leu Ile Phe Ile Ala Asn Ser Ile Asn Phe Ser Val Ile Ile
146                115                 120                 125
147    Phe Tyr Phe Arg Ile Phe Asn Gly Glu Asp Met Asn Gly Met Ser Leu
148        130                 135                 140
149    Trp
150    145
152 (2) INFORMATION FOR SEQ ID NO: 4:
154        (i) SEQUENCE CHARACTERISTICS:
155              (A) LENGTH: 140 amino acids
156              (B) TYPE: amino acid
157              (C) STRANDEDNESS: single
158              (D) TOPOLOGY: linear
160       (ii) MOLECULE TYPE: peptide
162      (vii) IMMEDIATE SOURCE:
163              (A) LIBRARY: GenBank
164              (B) CLONE: 1197072
166       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
168    Met Met Glu Phe Lys Val Ser Pro Leu Thr Lys Ile Ile Ser Leu Ser
169    1               5                  10                  15
170    Gly Phe Leu Ala Leu Gly Phe Leu Leu Val Ile Leu Ser Cys Ala Leu
171                20                  25                  30
172    Phe His Asn Tyr Tyr Pro Leu Phe Asp Ile Leu Ile Phe Leu Leu Ala
173                35                  40                  45
174    Pro Ile Pro Asn Thr Ile Phe Asn Ala Gly Asn Lys Tyr His Thr Ser
175        50                  55                  60
176    Asp Phe Met Ser Asp Ser Ser Asn Thr Gly Gln Asp Leu Ala His Phe
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```
177  65                      70                      75                      80
178  Leu Thr Gly Met Leu Val Thr Ser Gly Ile Ala Leu Pro Val Val Phe
179              85                      90                      95
180  Tyr His Cys Gln Leu Ile Gly His Leu Ser Cys Ile Met Cys Met Ile
181          100                     105                     110
182  Gly Gly Leu Ile Ile Tyr Ser Ser Ile Val Ile Phe Lys Trp Phe Phe
183          115                     120                     125
184  Lys Lys Asp Phe Asn Glu Asp Asp Ser Leu Phe Gly
185          130                     135                     140
```

VERIFICATION SUMMARY   DATE: 01/29/2002
PATENT APPLICATION: US/09/993,756A   TIME: 10:55:30

Input Set : **N:\Crf3\RULE60\09993756A.raw**
Output Set: **N:\CRF3\01292002\I993756A.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]